and/or chromosome 17 in humans, said method comprising [contacting] employing said chromosomal material [with] and a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases in in situ hybridization, wherein the chromosomal material is present in a morphologically identifiable chromosome or cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

48. (Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein the chromosomal material is present in a morphologically identifiable chromosome or cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

50. (Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein said targeted interphase chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said interphase

chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein the chromosomal material is present in a morphologically identifiable chromosome or cell nucleus; allowing said probe to bind to said targeted interphase chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target interphase chromosomal material.

Please add new claims as follows:

4 ~~51~~. The method of claim ~~48~~ 2, wherein the genetic rearrangement is a translocation or an inversion.

5 ~~52~~. The method of claim ~~48~~ 2, wherein the unique sequence high complexity nucleic acid probe is labeled.

6 ~~53~~. The method of claim ~~52~~ 5, wherein said labeled unique sequence high complexity nucleic acid probe comprises fragments complementary to a single chromosome, fragments complementary to a subregion of a single chromosome, fragments complementary to a genome or fragments complementary to a subregion of a genome.

7 ~~54~~. The method of claim ~~48~~ 2, wherein the interphase chromosomal material is interphase chromosomal DNA.

8 ~~55~~. The method of claim ~~50~~ 3, wherein the genetic rearrangement is a translocation or an inversion.

9 ~~56~~. The method of claim ~~50~~ 3, wherein the unique sequence high complexity nucleic acid probe is labeled.